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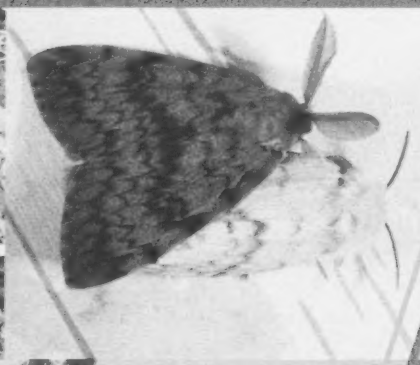

RESEARCH AT THE CANADIAN WOOD FIBRE CENTRE AND LAURENTIAN FORESTRY CENTRE OF NATURAL RESOURCES CANADA

Forest genomics

Canada

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What is genomics?

All living organisms contain DNA. DNA comprises a set of four nitrogenous bases (represented by the letters A, T, G and C). The order in which these four letters are put together "make up words and sentences" (genes), thereby "writing a book" (the genome), which includes billions of letters. The genome (a term derived from *gene* and *chromosome*) compiles all the genetic information contained in each cell of a living organism. It can thus be compared to an instruction manual, enabling cells to perform their various functions.

Genomics is the study of living organisms' genetic material, both in its structure and in its functions. Over the past twenty years, this science has advanced remarkably with the progress of sequencing techniques aimed at decoding DNA. Its applications help advance knowledge in a variety of sectors such as human health, agri-food, fishing and aquaculture, mining, energy, environment, and... forestry!

WHICH IS MORE COMPLEX, THE WHITE SPRUCE OR A HUMAN BEING?

Surprisingly, the white spruce genome is more complex than that of a human being. The former has approximately 20,000 megabases*, while the latter has roughly 3,000 megabases.

Other examples of sequenced genomes include:

- Poplar - 520 megabases
- Spruce budworm - 450 megabases
- Blister rust - 100 megabases

** 1 megabase = 100 million nitrogenous bases*

SEQUENCING AND BIOINFORMATICS FOR DECODING DNA

To decipher the structure (order and organization) of the four letters (A, T, C and G) in a specific organism's genome, it must be sequenced or "read". Given the size of genomes, this generates a significant amount of data.

Powerful computers and bioinformatics tools are therefore necessary to analyze the data. Genomes can then be deciphered and scrutinized. It is even possible to compare genomes (in part or in whole) to identify differences existing between individuals and between species.

Bioinformatics thus uses computer science for the benefit of biological sciences to collect and analyze genomics data.

Genomics in forestry

Genomics makes it possible to develop tools for the selection of better-performing trees and trees that are more adapted to their environment, that better meet the forestry sector s needs or that can be used in the reforestation of disturbed sites, for example. Genomics also aims to identify, detect and control forest pests, and to validate the origin of the wood.

Research teams at the Laurentian Forestry Centre (LFC) and the Canadian Wood Fibre Centre (CWFC), two research centres at Natural Resources Canada s Canadian Forest Service (CFS), are at the forefront of research and technological transfer in these various areas. The following is an overview of the work that is being conducted.

INCREASING WOOD VALUE

In close collaboration with FPInnovations, the CWFC is developing innovative skills and technologies so as to increase economic opportunities for Canadian wood in all its forms. CWFC specialists across Canada are working on tree improvement, vegetation management, innovative silvicultural approaches and wood characterization, while developing expertise in technological transfer and development.

For further information: *cwfc.nrcan.gc.ca*

Genomic selection for reforestation

The different spruce species account for more than half of the wood volume harvested and used by the Canadian forest industry (pulp and paper, timber). White spruce is especially valuable in reforestation projects due to its interesting traits, which include strong growth, good wood quality, and low susceptibility to pests. The genome of this species has been entirely deciphered, which is why the white spruce improvement program is one of the most advanced in Canada. This program uses genome portions (markers) associated with certain tree characteristics to select white spruce trees that perform better (growth and wood quality) or show a greater capacity to adapt to different environmental conditions (drought, disease).

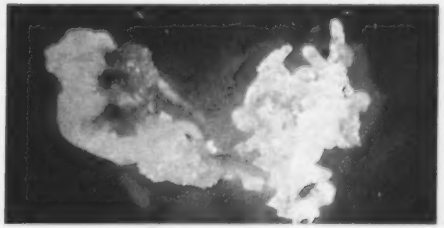
CFS research teams combine traditional tree selection approaches, such as physiology and dendroecology (study of the relationship between trees and their habitat over time), to genomic approaches in order to identify the genetic markers linked to tree characteristics. As marker-assisted selection can be carried out at any stage of tree development, promising seedlings can be identified as early as during their first years of growth. This prevents having to wait 20 or 30 years to assess the potential of a tree, as is the case with traditional genetic improvement programs. In addition, trees can be identified by their genetic imprints (barcodes) rather than by their physical characteristics.

Simply put, this approach helps select and then reproduce (through crossing or embryogenesis) plants with desirable characteristics, such as:

- a better adaptation to changing environmental conditions;
- quality attributes (upright growth, fewer branches, cylindrical trunk, greater density, etc.) for the current and future needs of the forestry sector;
- increased resistance to insects and diseases.

COPY-PASTING A TREE

What if we could use a single seed from a tree considered to be exceptional due to its wood, appearance and resistance to rapidly produce a series of identical specimens of the same quality? This can be done by combining genomic selection with somatic embryogenesis, a plant cloning method. Using this method, scientists produce a multitude of embryos from a single seed in a laboratory setting; these embryos then become genetically identical trees. Genomic selection accelerates the process by allowing researchers to identify the embryos to be cloned without having to wait for several years of growth. The CFS is a world leader with regard to applying the somatic embryogenetic protocol to numerous species.



THE FASTTRAC PROJECT: COMING UP WITH FAST SOLUTIONS!

Year after year, over 400 million spruce seedlings are planted in Canada. Genetic improvement programs provide high-performing seedlings for reforestation, particularly in terms of growth. Complex characteristics, such as wood quality and pest resistance, are also sought after.

CFS research teams, in collaboration with different partners (Université Laval, FPInnovations, Génome Québec, Genome Atlantic, Genome Canada, the New Brunswick Tree Improvement Council, JD Irving, and the ministère des Forêts, de la Faune et des Parcs du Québec) are developing rapid tests to select spruce with the desired wood characteristics with the help of genomics. These diagnostic tools make it possible to predict the genetic value of a tree right at the seedling stage rather than having to wait for a field study that can last as long as 30 years for certain characteristics. Genomics-based selection models will help characterize thousands of white spruce and Norway spruce according to their growth potential, wood density, or resistance to insects or disease. Thanks to genomics, trees with the desired characteristics can be planted much sooner and their value could increase by as much as 20% over time, which represents a potential added value of close to $300 million per year for Canada's forest sector.

For further information:
fasttracproject.ca/en/home

PROJET FastTRAC PROJECT
Tests rapides pour l'amélioration des conifères | Fast Tests for Rating and Amelioration of Conifers

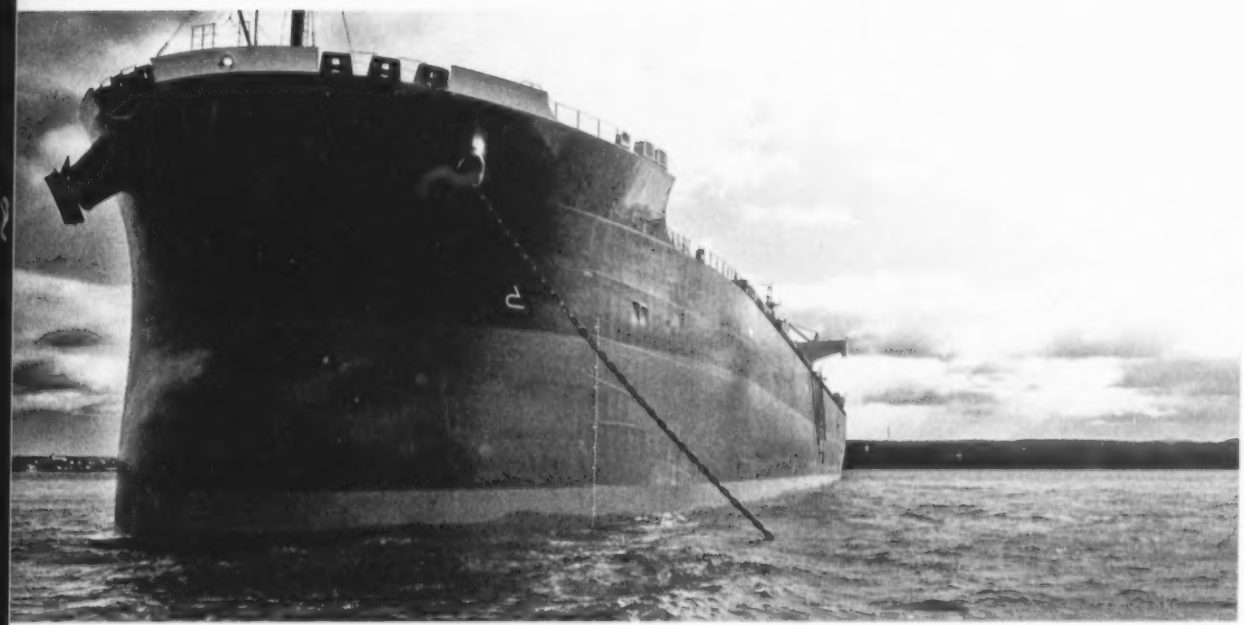
Génome Québec : dossier spécial sur le projet FastTRAC (available in French only)
genomequebec.com/282-nouvelle-genomique-forestiere-dossier-special-sur-le-projet-fasttrac-dans-lapresse-.html

Pest identification, detection and control methods

Insects and diseases affect thousands of hectares of forest annually, causing significant economic and environmental losses. In Canada, the revenue loss and cost of prevention, control and risk mitigation measures implemented over the years are estimated to be in the hundreds of millions of dollars. Furthermore, due to the growing international trade, the risk of harmful exotic species being introduced looms over Canadian forests.

Thankfully, genomics makes it possible to develop additional tools to identify, detect and control forest pests. Indeed, it helps to quickly identify certain species, better understand and counter pests' strategies, and improve our knowledge of trees' molecular defence mechanisms.

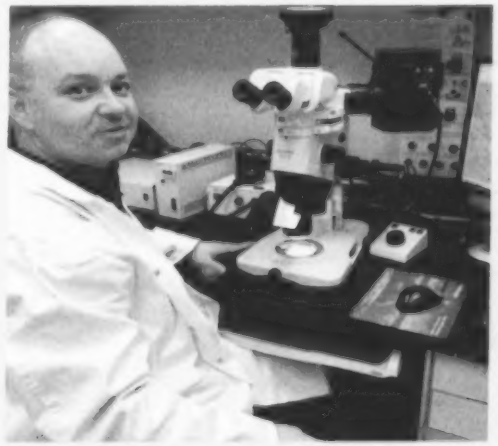
One of the difficulties researchers encounter when working on pest control is identifying the species and discriminating among related species. At certain stages of the development (egg, larva), the identification of insects can be challenging, if not impossible. Many disease-causing pathogens have very few distinguishable morphological characteristics (colour, shape, specific traits, etc.), and the diseases they cause do not always have obvious signs or symptoms in the short term.

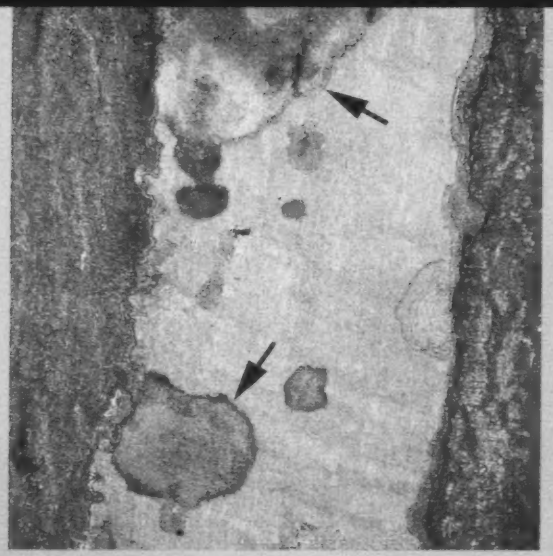


A GENETIC BARCODE

Just like the barcodes on the products we purchase in stores, genetic barcodes differentiate one species from another. Each species and each variety are characterized by unique DNA segments. Researchers the world over, many of whom are with the CFS, are working towards decoding these identifiers for living organisms. Once the barcodes are decoded, they are entered into an international catalogue that contains data related to all living organisms. Any scientist can consult this database and quickly identify an organism.

If the species to which the organism belongs has been identified, its profile will be available. This is how CFS research teams were able to state beyond a doubt that the dreaded fungus *Melampsora pinitorqua* Rostr., a species of poplar rust that cannot be distinguished from related species under a microscope, had not entered into Canada. The genetic barcode of this fungus is now being used as a tool to assess suspect imported plants.





Using genomics, CFS researchers can now quickly identify different pest species. By identifying genome portions specific to certain species, CFS scientists develop detection tools for the early identification of certain forest pests. These tests are quick, simple and inexpensive. They are based on the genetic imprint of the targeted species and can distinguish between harmless species and those that can cause major damage. CFS researchers have thus developed one of the first tests that can track the fungus *Phytophthora ramorum*, the pathogen responsible for sudden oak death. This disease's symptoms vary from one species to the next, and it attacks a hundred or so North American and European plant species, including several tree species. Since the pathogen responsible for this disease is not yet established in Canada, it is being monitored closely by the Canadian Food Inspection Agency (CFIA). The CFIA uses the detection tools developed by the CFS to quickly intervene in case it is introducted into Canada.

It is also possible to detect the presence of pests more indirectly by detecting molecular defence signals in trees. Indeed, attacks by insects or pathogens cause a defence reaction in trees, which is itself dictated by the tree's genome. This reaction can be detected using genomics and can be used as an additional detection tool.

Finally, genomics is used to better control pests by increasing our understanding of the genes involved in the basic biological functions of pests (including winter survival and reproduction) or those that allow pests to attack trees. This knowledge makes it possible to develop strategies to counter such attacks. Moreover, it is possible to identify the genes that induce natural resistance to a specific pest by studying the molecular defence mechanisms of trees. Research teams can then select trees that are more resistant using genomic selection.

ASIA OR EUROPE?

The Asian gypsy moth is one of the top priority exotic pests being studied at the CFS, and with good reason! This insect, which is well adapted to cold, attacks over 500 tree species. Female Asian gypsy moths are capable of flight and can rapidly colonize a large area, unlike female European gypsy moths. The introduction of the Asian gypsy moth could thus cause significant socioeconomic and environmental damage. It is not yet established in Canada; however, egg masses have been detected a number of times on ships arriving at Canadian ports.

A simple visual inspection of the egg masses or young larvae is not sufficient to distinguish the Asian gypsy moth from its European counterpart, which is already established in North America. Research teams at the CFS and their partners have created a database of Asian gypsy moth and related species DNA markers in order to develop a series of molecular detection tests specific to the Asian gypsy moth, to the European gypsy moth, or to one of the five other species of exotic gypsy moths that constitute a threat to Canada's forests. The CFIA uses this set of genomic tools to identify this invasive insect species in Canadian ports. Quarantine measures may therefore be imposed by the competent authorities, if necessary.

IN A RUSH TO HEAD OFF RUST!

White pine blister rust, which is caused by the fungus *Cronartium ribicola*, is another insidious pest. This disease was introduced into North America in the early 20th century on white pine seedlings imported from Europe. Today, it affects 90% of Quebec's white pine plantations and can cause significant mortality. Every year, millions of white pine seedlings are used for reforestation purposes. Nurseries have implemented measures to prevent rust infection. However, despite these precautions, infected seedlings may sometimes be planted since the disease is asymptomatic for the first few years following infection. To solve this problem, CFS research teams have developed a test based on the genetic imprint of the pathogen to detect its presence in tree or seedling tissues. This test was introduced in 2011 and is used to support the issuance of phytosanitary certificates for white pine seedlings produced at six forest nurseries in Quebec.

ANNOSUM ROOT DISEASE INFESTATION

Annosum root disease has been present in Quebec since 1989. It namely affects pines in plantations undergoing thinning operations. Spores of the fungus *Heterobasidion irregulare* enter through freshly-cut stumps and infect healthy trees by root contact, resulting in considerable financial losses. The fungus can survive for a very long time in stumps and roots: over half a century! CFS research teams have developed molecular tools to detect and assess the presence of airborne spores and thereby estimate the risk of infection for a given territory. This makes it possible to react quickly in the event of an infection, before it is too late to stop it.

THE TAIGA PROJECT: PROTECTING THE FOREST

To prevent the introduction and spread of diseases, researchers from the CFS and from several partner institutions (University of British Columbia, Simon Fraser University, Michael Smith Genome Sciences Centre, CFIA, FPInnovations, Boreal Genomics, Genome BC and Genome Canada) have combined their efforts to develop more effective tools for the detection and monitoring of exotic pathogens based on their genetic imprint. CFS research teams have developed over 50 molecular screening tests that target exotic species that are not established in Canada. These tools were then transferred to the CFIA, enabling the agency to take action rapidly in the event that diseases are introduced in Canada. Thanks to genomics, pathogens are being monitored closely!

taigaforesthealth.com

TAIGA
FOREST HEALTH

UNMASKING THE INTRUDER

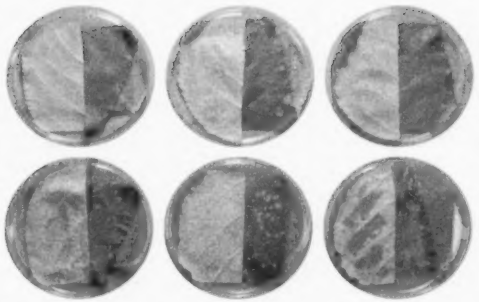
Since its appearance in Canada in 2002, the emerald ash borer has already killed millions of ash trees. CFS scientists estimate that the cost of treating, cutting, and replacing the trees affected by this exotic insect could reach $2 billion in Canada over three decades. The challenge? Detecting the insect at an early stage. Trees that have been recently attacked by the emerald ash borer do not exhibit any symptoms and, for the moment, there is no method to detect infestation quickly. Indigenous ash trees do not appear to have developed any natural resistance to this pest. However, researchers know that any attack on a tree causes a defence reaction. CFS researchers are attempting to identify and characterize this molecular response in ash trees under attack by the ash borer in order to use it as an indicator of the pest's presence before the tree shows any symptoms. This knowledge could also be used in ash tree genetic improvement programs and in the development of new tools to control the ash borer.

REDUCING THE DAMAGE

Spruce budworm (SBW) epidemics are the most significant natural disturbance affecting Canadian fir forests. In eastern Canada, the SBW destroys as many trees as forest fires do. A new epidemic has been raging in Quebec and New Brunswick since 2006. In 2017, the budworm defoliated over 3.4 million hectares of forest in the North Shore region of Quebec, a territory the size of Belgium!

In order to optimize current strategies aiming to control the damage caused by the SBW, CFS research teams are working on analyzing this insect's genome. They are particularly interested in specific genes that could be used to develop control tools. For example, genes associated with the insect's winter survival could be blocked to increase its mortality rate during the cold season.

POPLAR LEAF RESPONSE TO RUST INFECTION



RUSTED POPLARS

Poplar leaf rust, caused by different species of the *Melampsora* fungus, is one of the most damaging forest diseases in the world. CFS scientists have noted that poplars have a certain level of natural resistance to blister rust in their genetic baggage. However, this protection is often specific to a particular pathogen and over time, it can be thwarted by the fungus. CFS scientists have therefore searched for resistance genes in the genome of poplars that would not be specific to a single species of blister rust. Thanks to genomics, they have identified 26 genes linked to resistance to several species of blister rust. This discovery could help produce poplars with an increased and durable resistance to these pathogenic fungi.

Moreover, by studying the response of poplar leaves to rust infection, CFS researchers have noticed that the tree secretes a protein with antifungal properties, which stops the germination of fungal spores on the leaves. By further studying this protein, scientists hope to better understand the tree's defence mechanisms and, ultimately, to use them to control this disease. At present, researchers are relying on molecular detection tools to identify fungal species found on poplars that also infect other species, such as larches, pines and various herbaceous plants.

PROVIDING WEAPONS TO THE BUTTERNUT

Butternut canker is a threat to the survival of this tree species. In Quebec, the fungus was reported for the first time in 1990. The low genetic variability and very high level of virulence characterizing the fungus (*Ophiognomonia clavigignenti-juglandacearum* – OCJ) indicate that it is most probably an exotic pest. The fungus is carried from tree to tree by wind, rain and possibly by a variety of insects. The cankers caused by the infection first appear in the crown of the tree, then spread downward. Over time, the disease kills the affected branches and, when it girdles the trunk, the tree dies.

To support the management of this disease, genomics has made it possible to develop molecular tests to assess fungal sporulation in the trees studied. These quantitative tests, which are sensitive enough to detect a single OCJ spore, have made it possible to assess the efficacy of different silvicultural treatments aiming to favour tree vigour and identify those that are the most effective.

Also, researchers have found that some butternut trees appear to have a certain level of resistance to the disease. Before exploring this resistance further, they wanted to make sure that the trees had been correctly identified. Indeed, as the Japanese walnut, an exotic species, also shows a certain resistance to OCJ and is known to form hybrids with the butternut, researchers wanted to be able to detect the presence of hybridization between both species. To do so, molecular tools were developed to enable the rapid detection of hybrids. These tools help verify that resistant butternuts are actually pure butternuts (native species) and not hybrids combining butternut and Japanese walnut characteristics. This reliable characterization of hybrids will facilitate future research on the resistance to OCJ in butternut trees and could eventually help reestablish the species, which has been protected under the *Species at Risk Act* since 2005.

The impact of climate change

Like the entire planet, Canada s forests must deal with climate change. Seing as Canada is a northern country, scientists expect climate disruptions to be more pronounced here compared with the worldwide average.

Under these circumstances, genomics can be a valuable tool for producingmore accurate assessments of the impacts of climate change on forest productivity and can contribute to adaptation solutions. Current models assume that all trees have the same response to climate-related events, which is far from reality. By integrating the genomic variability of trees into these models, scientists will be able to characterize tree populations according to their response to a certain type of change (e.g., frost, drought, increased concentration of carbon dioxide), among other things. This means it will be easier to select seedlings for reforestation or to protect certain species, depending on the climate conditions that are expected in 10, 20 or 30 years.

Support in forest certification

The various species of poplar can easily form hybrids with one another. Hybridization is the result of a cross between two different species (exotic or indigenous); it generates hybrids that possess the characteristics of both parent trees. Studies conducted by CFS research teams have shown that exotic poplars (i.e., those originating from another country), some of which were introduced over 300 years ago, could form hybrids with indigenous poplars.

Due to their strong growth potential, hybrid poplars with exotic components are used more and more frequently in plantations around the world, particularly for biomass production. They are also valued as windbreaks on farmlands. This is the reason why (exotic) Russian poplars, some of which were already hybrids, were crossed with (indigenous) Eastern cottonwood in the Prairies. These new hybrid varieties are known for their ability to adapt to extreme continental climate conditions.

However, certain forest certification standards and provincial regulations limit the planting of hybrid poplars or poplars with exotic components. The goal is to limit the spread of these characteristics within the natural regeneration. Given the situation, the challenge is to accurately identify these characteristics in order to be able to monitor and, especially, to control their spread. The exchange of genetic material that occurs when different species hybridize makes this identification very difficult, especially when the species share the same habitat. However, CFS experts have developed a diagnostic tool that uses genetic markers to distinguish the ten poplar species (exotic and indigenous) most commonly found in North America, as well as their hybrids. Monitoring their spread has thus been greatly facilitated.

Restoration of disturbed sites

The combination of human activities and climate change can affect soil quality and productivity. One of the solutions being considered by scientists to restore land that has been disturbed by the development of natural resources, for example, is to make use of the microorganisms (microbiome) present in the soil. These play a vital role in the nitrogen and carbon cycles, help plants better assimilate certain nutrients, and are involved in the breakdown of complex compounds, including certain pollutants such as hydrocarbons. This last function is called phytoremediation.

Research teams at the CFS use genomics to compare the undisturbed soil microbiome with that from environments disturbed by various human activities. By identifying the species present and studying their role based on the soil characteristics, it is possible to identify biological indicators of environmental stresses. These indicators are then used to better predict the impact of various disturbances and follow up on the restoration of disturbed sites. These studies also make it possible to identify the best plant/microorganism combinations to restore disturbed sites.

Genomics and the economy

CFS scientists are relying on transferring knowledge to different partners (e.g., forest nurseries, provincial departments, regulatory agencies) in order to reduce the financial losses caused by insects, diseases and the climate, and to increase the value of the forest. Molecular markers and the genetic barcodes obtained from genomic studies are among the tools used to:

- support forest management efforts in Canada;
- diversify products for international markets;
- produce and harvest quality wood fibre;
- accelerate the identification of sought-after wood traits;
- prevent the introduction and counter the impact of forest pests;
- mitigate the impact of climate change and adapt to it;
- strengthen Canada's environmental leadership.

The future of genomics research

Collaboration is at the heart of Canadian forestry genomics strategies and successes. In this regard, CFS research teams are involved in the large-scale projects presented on the following page.

DESCRIPTION	MAIN INSTITUTIONS	PARTNERS
SPRUCE-UP: FURTHER IMPROVING SPRUCE TREES The genetic improvement of white spruce intended for reforestation aims to develop trees that are better adapted to climate change. Desired traits include resistance to insects and drought, the efficient use of nutrients, as well as improved wood quality and growth.	• University of British Columbia • Université Laval	CFS, Geological Survey of Canada, BC Ministry of Forests, Lands and Natural Resources, Ministère des Forêts, de la Faune et des Parcs du Québec, University of Oxford, Max Planck Institute for Chemical Ecology, Precision Hawk, University of Alberta, FPInnovations, Joint Genome Institute (US Department of Energy), University of Toronto, Alberta Innovates, Alberta Agriculture and Forestry, Genome BC, Genome Prairies, Genome Québec, Genome Canada.
BIOSAFE: MONITORING INVASIVE EXOTIC SPECIES Invasive exotic species, such as the Asian longhorned beetle, Dutch elm disease, sudden oak death and Asian gypsy moth, are threatening Canadian forests. A new set of tools will make it possible to detect them more effectively and identify their geographical origin as well as their introduction pathway. This work will lead to quicker intervention by containing the threats at their source.	• University of British Columbia • Université Laval • CFIA	CFS, FPInnovations, McGill University, University of Victoria, University of Western Ontario, BC Ministry of Forests, Lands and Natural Resources, Ministère des Forêts, de la Faune et des Parcs du Québec, Manitoba Conservation and Water Stewardship, Agriculture and Agri-Food Canada, Forest Service Branch - Saskatchewan Government, Alberta Agriculture and Forestry, Genome BC, Genome Québec, Genome Canada.
COADAPTREE: HEALTHY TREES TO ADAPT TO FUTURE CLIMATE CONDITIONS Researchers are working on better reforestation options for high-yield species such as Douglas-fir, shore pine, western larch and jack pine. The project will use genomic tools in combination with experiments to test the resistance of trees to heat, cold, and stress caused by drought and diseases.	• University of British Columbia • University of Calgary • Université Laval	CFS, University of Toronto, University of Victoria, University of Alberta, BC Ministry of Forests, Lands and Natural Resources, Alberta Environment & Sustainable Resource Development, Alberta Tree Improvement & Seed Centre, Western Forest Products, Timberwest, BC Forest Genetics Council, SelectSeed Ltd., USDA Forest Service, Swiss Federal Research Institute, Vernon Seed Orchard Company, Compute Canada, Genome BC, Genome Québec, Genome Alberta, Genome Canada.
RESISTANT FORESTS (RES-FOR): ADDRESSING THREATS The RES-FOR project aims to use metabolic profiling and mathematical modelling in current genetic selection programs in order to produce trees that are resistant to insect epidemics and droughts, and that also have better wood quality.	• University of Alberta • University of British Columbia	CFS, University of Calgary, Alberta Innovates, Blue Ridge Lumber Inc., Hinto Wood Products, Alberta Agriculture and Forestry, Weyerhaeuser, Forest Resource Improvement Association of Alberta, Genome Alberta, Genome BC, Genome Canada.
ECOBIOMICS: STUDYING DISTURBED SITES This project uses genomics to assess soil and water biodiversity in different ecosystems. This will then be used to measure the impact of natural resources development on ecosystem biodiversity and integrity. Water and soil microbiomes, as well as aquatic invertebrates, will be studied at various sites across the Great Lakes region (Ontario), the boreal forest of Ontario and Quebec, and the oil sands region, including the Peace-Athabasca Delta (Alberta).	• CFIA • National Research Council of Canada • Environment and Climate Change Canada • Fisheries and Oceans Canada • Public Health Agency of Canada • Agriculture and Agri-Food Canada	CFS, several municipalities (Clarenceville, St-Armand, Venise-en-Québec, Pike River), Direction de la santé publique du Québec, Ministère du Développement durable, de l'Environnement et de la Lutte contre les changements climatiques du Québec, Université de Montréal, Université du Québec à Montréal, University of British Columbia, Alberta Environmental Monitoring, Evaluation and Reporting Agency, University of Waterloo, Oregon State University, National Ecological Observatory Network (NEON), Ontario Ministry of the Environment and Climate Change, Ontario Ministry of Agriculture, Food and Rural Affairs, Ontario Ministry of Natural Resources and Forestry, Ontario Soil and Crop Improvement Association, Prince Edward Island Department of Agriculture and Fisheries, University of Prince Edward Island, Tembec, Resolute Forest Products, Sustainable Forestry Initiative, Laurentian University, JD Irving Ltd., University of New Brunswick, University of Toronto.

For further information

VIDEOS

What can genomics do for Canada's forestry sector?
Natural Resources Canada video
nrcan.gc.ca/forests/video/17158

Forest genetics
FPInnovations video
youtube.com/watch?v=X7DADlgWdG8

Genomics and the forestry sector
Genome Canada/Genome BC video
youtube.com/watch?v=aVmRgejbEng

Les gènes de nos forêts
Video by Marine Vautier, Ph. D. student (Université Laval) (available in French only)
youtube.com/watch?v=jui61dN-s3A

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